

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> NOVEL bHLH TYPE TRANSCRIPTION FACTOR GENES DEC2

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<150> JP 1999-233286

<151> 1999-08-19

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<170> PatentIn Ver. 2.1

<210> 1

<211> 3641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (135)..(1580)

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aacagcagtt gaac atg gac gaa gga att cct cat ttg caa gag aga cag 170

Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln

1 5 10

tta ctg gaa cat aga gat ttt ata gga ctg gac tat tcc tct ttg tat 218

Leu Leu Glu His Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr

15 20 25

atg tgt aaa ccc aaa agg agc atg aaa cga gac gac acc aag gat acc 266

Met Cys Lys Pro Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Asp Thr

30 35 40

tac aaa tta ccg cac aga tta ata gaa aag aaa aga aga gac cga att 314

Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile

45 50 55 60

aat gaa tgc att gct cag ctg aaa gat tta ctg cct gaa cat ctg aaa 362

Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys

65 70 75

ttg aca act ctg gga cat ctg gag aaa gct gta gtc ttg gaa tta act 410
 Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr

80 85 90

ttg aaa cac tta aaa gct tta acc gcc tta acc gag caa cag cat cag 458
 Leu Lys His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln

95 100 105

aag ata att gct tta cag aat ggg gag cga tct ctg aaa tcg ccc att 506
 Lys Ile Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile

110 115 120

cag tcc gac ttg gat gcg ttc cac tcg gga ttt caa aca tgc gcc aaa 554
 Gln Ser Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys

125 130 135 140

gaa gtc ttg caa tac ctc tcc cgg ttt gag agc tgg aca ccc agg gag 602
 Glu Val Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu

145 150 155

ccg cgg tgt gtc cag ctg atc aac cac ttg cac gcc gtg gcc acc cag 650
 Pro Arg Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln

160 165 170

ttc ttg ccc acc ccg cag ctg ttg act caa cag gtc cct ctg agc aaa 698

Phe Leu Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys

175

180

185

ggc acc ggc gct ccc tcg gcc ggg tcc gcg gcc gcc ccc tgc ctg 746

Gly Thr Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu

190

195

200

gag cgc gcg ggg cag aag ctg gag ccc ctc gcc tac tgc gtg ccc gtc 794

Glu Arg Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val

205

210

215

220

atc cag cgg act cag ccc agc gcc gag ctc gcc gcc gag aac gac acg 842

Ile Gln Arg Thr Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr

225

230

235

gac acc gac agc ggc tac ggc ggc gaa gcc gag gcc cgg ccg gac cgc 890

Asp Thr Asp Ser Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg

240

245

250

gag aaa ggc aaa ggc gcg ggg gcg agc cgc gtc acc atc aag cag gag 938

Glu Lys Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu

255

260

265

cct ccc ggg gag gac tcg ccg gcg ccc aag agg atg aag ctg gat tcc 986

Pro Pro Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser

270

275

280

cgc ggc ggc ggc agc ggc ggc ccg ggg ggc ggc gcg gcg gcg gcg 1034
 Arg Gly Gly Gly Ser Gly Gly Pro Gly Gly Ala Ala Ala Ala
 285 290 295 300

gca gcc gcg ctt ctg ggg ccc gac cct gcc gcc gcg gcc ctg ctg 1082
 Ala Ala Ala Leu Leu Gly Pro Asp Pro Ala Ala Ala Ala Leu Leu
 305 310 315

aga ccc gac gcc gcc ctg ctc agc tcg ctg gtg gcg ttc ggc gga ggc 1130
 Arg Pro Asp Ala Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly
 320 325 330

gga ggc gcg ccc ttc ccg cag ccc gcg gcc gcc gcg gcc ccc ttc tgc 1178
 Gly Gly Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Pro Phe Cys
 335 340 345

ctg ccc ttc tgc ttc ctc tcg cct tct gca gct gcc gcc tac gtg cag 1226
 Leu Pro Phe Cys Phe Leu Ser Pro Ser Ala Ala Ala Tyr Val Gln
 350 355 360

ccc ttc ctg gac aag agc ggc ctg gag aag tat ctg tac ccg gcg gcg 1274
 Pro Phe Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala
 365 370 375 380

gct gcc gcc ccg ttc ccg ctg cta tac ccc ggc atc ccc gcc ccg gcg 1322

Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala

385 390 395

gca gcc gcg gca gcc gcc gcc gct gcc gcc gcc gcc gcc gcg ttc 1370

Ala Phe

400 405 410

ccc tgc ctg tcc tcg gtg ttg tcg ccc cct ccc gag aag gcg ggc gcc 1418

Pro Cys Leu Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala

415 420 425

gcc gcc gcg acc ctc ctg ccg cac gag gtg gcg ccc ctt ggg gcg ccg 1466

Ala Ala Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro

430 435 440

cac ccc cag cac ccg cac ggc cgc acc cac ctg ccc ttc gcc ggg ccc 1514

His Pro Gln His Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro

445 450 455 460

cgc gag ccg ggg aac ccg gag agc tct gct cag gaa gat ccc tcg cag 1562

Arg Glu Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln

465 470 475

cca gga aag gaa gct ccc tgaatccttg cgtcccgaaag gacggagggtt 1610

Pro Gly Lys Glu Ala Pro

480

caagcagagt gagaagttaa aataccctta aggaggttca agcagagtga gaagttaaaa 1670

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gacatggaac agcaggtagt tgttatgtag agctagttct caaagctgcc ctgcctgttt 2090

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<211> 482

<212> PRT

<213> Homo sapiens

<400> 2

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1

5

10

15

Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20	25	30
----	----	----

Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro

35	40	45
----	----	----

His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile

50	55	60
----	----	----

Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu

65	70	75	80
----	----	----	----

Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu

85	90	95
----	----	----

Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala

100	105	110
-----	-----	-----

Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser Asp Leu

115	120	125
-----	-----	-----

Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln

130	135	140
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Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Val

145

150

155

160

Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu Pro Thr

165

170

175

Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr Gly Ala

180

185

190

Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg Ala Gly

195

200

205

Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln Arg Thr

210

215

220

Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr Asp Ser

225

230

235

240

Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys Gly Lys

245

250

255

Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro Gly Glu

260

265

270

Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly Gly

275

280

285

Ser Gly Gly Gly Pro Gly Gly Ala Ala Ala Ala Ala Ala Leu

290 295 300

Leu Gly Pro Asp Pro Ala Ala Ala Ala Leu Leu Arg Pro Asp Ala

305 310 315 320

Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly Ala Pro

325 330 335

Phe Pro Gln Pro Ala Ala Ala Ala Pro Phe Cys Leu Pro Phe Cys

340 345 350

Phe Leu Ser Pro Ser Ala Ala Ala Tyr Val Gln Pro Phe Leu Asp

355 360 365

Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala Ala Pro

370 375 380

Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala Ala Ala

385 390 395 400

Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu Ser

405 410 415

Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala Thr

420 425 430

Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro Gln His

435

440

445

Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu Pro Gly

450

455

460

Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly Lys Glu

465

470

475

480

Ala Pro

<210> 3

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

<400> 4

gcaagtgggtt gatcagctgg acaca

25

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

<400> 5

gcttacccat acgatgttcc a

21

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 6

tggaacgcat ccaagtcgga ctgaat

26

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 7

ttgaacatgg acgaaggaat tcc

23

<210> 8

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 8

gagatggtgc acgatgcaca gttgaagtga ac 32

<210> 9

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 9

attcagtcgg acttgatgc gttcca 26

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

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gcgggggtttt tcagtatcta cga

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<210> 11

<211> 1511

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1453)

<400> 11

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Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His

1

5

10

15

aga gat ttt ata gga ctg gac tat tcc tct ttg tat atg tgt aaa ccc 97

Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20

25

30

aaa agg agc atg aaa cga gac gac acc aag gta agt gat acc tac aaa 145

Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Val Ser Asp Thr Tyr Lys

35

40

45

tta ccg cac aga tta ata gaa aag aaa aga aga gac cga att aat gaa 193

Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu

50

55

60

tgc att gct cag ctg aaa gat tta ctg cct gaa cat ctg aaa ttg aca 241

Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr

65

70

75

80

act ctg gga cat ctg gag aaa gct gta gtc ttg gaa tta act ttg aaa 289

Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys

85

90

95

cac tta aaa gct tta acc gcc tta acc gag caa cag cat cag aag ata 337

His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile

100

105

110

att gct tta cag aat ggg gag cga tct ctg aaa tcg ccc att cag tcc 385

Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser

115

120

125

gac ttg gat gcg ttc cac tcg gga ttt caa aca tgc gcc aaa gaa gtc 433

Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val

130

135

140

ttg caa tac ctc tcc cgg ttt gag agc tgg aca ccc agg gag ccg cgg 481

Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg

145

150

155

160

tgt gtc cag ctg atc aac cac ttg cac gcc gtg gcc acc cag ttc ttg 529

Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu

165

170

175

ccc acc ccg cag ctg ttg act caa cag gtc cct ctg agc aaa ggc acc 577

Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr

180

185

190

ggc gct ccc tcg gcc gcc ggg tcc gcg gcc gcc ccc tgc ctg gag cgc 625

Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg

195

200

205

gcg ggg cag aag ctg gag ccc ctc gcc tac tgc gtg ccc gtc atc cag 673

Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln

210

215

220

cg^g ac^t ca^g cc^c ag^c gc^c ga^g ct^c gc^c ga^g aa^c ga^c ac^g ga^c ac^c 721

Arg Thr Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr

225

230

235

240

ga^c ag^c gg^c ta^c gg^c gg^c ga^a gg^c ga^g gg^c cg^g ga^c cg^c ga^g aa^a 769

Asp Ser Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys

245

250

255

gg^c aa^a gg^c gc^g gg^g gg^c ag^c cg^c gt^c ac^c at^c a^a g^a ca^g ga^g cc^c cc^c 817

Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro

260

265

270

gg^g ga^g ga^c tc^g cc^g gc^g cc^c a^a g^g at^g a^a g^t ct^g ga^t tc^c cg^c gg^c 865

Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly

275

280

285

gg^c gg^c ag^c gg^c gg^c gg^c cc^g gg^g gg^c gg^c gg^c gg^c gg^c gca^g cc^c 913

Gly Gly Ser Gly Gly Pro Gly Gly Ala Ala Ala Ala Ala

290

295

300

gc^g ct^t ct^g gg^g cc^c ga^c ct^c gc^c gc^c gc^c gc^c ct^g ct^g ag^a cc^c 961

Ala Leu Leu Gly Pro Asp Pro Ala Ala Ala Ala Leu Leu Arg Pro

305

310

315

320

gac gcc gcc ctg ctc agc tcg ctg gtg gcg ttc ggc gga ggc ggc 1009

Asp Ala Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly

325

330

335

gcg ccc ttc ccg cag ccc gcg gcc gcc ggc ccc ttc tgc ctg ccc 1057

Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Pro Phe Cys Leu Pro

340

345

350

ttc tgc ttc ctc tcg cct tct gca gct gcc gcc tac gtg cag ccc ttc 1105

Phe Cys Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln Pro Phe

355

360

365

ctg gac aag agc ggc ctg gag aag tat ctg tac ccg gcg gcg gct gcc 1153

Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala

370

375

380

gcc ccg ttc ccg ctg cta tac ccc ggc atc ccc gcc ccg gcg gca gcc 1201

Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala

385

390

395

400

gcg gca gcc gcc gcc gct gcc gcc gcc gcc ggc ttc ccc tgc 1249

Ala Phe Pro Cys

405

410

415

ctg tcc tcg gtg ttg tcg ccc cct ccc gag aag gcg ggc gcc gcc gcc 1297

Leu Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala

420	425	430
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gcg acc ctc ctg ccg cac gag gtg gcg ccc ctt ggg gcg ccg cac ccc 1345

Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro

435	440	445
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cag cac ccg cac ggc cgc acc cac ctg ccc ttc gcc ggg ccc cgc gag 1393

Gln His Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu

450	455	460
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ccg ggg aac ccg gag agc tct gct cag gaa gat ccc tcg cag cca gga 1441

Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly

465	470	475	480
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aag gaa gct ccc tgaatccttg cgtcccgaag gacggagggtt caagcagagt 1493

Lys Glu Ala Pro

gagaagttaa aataccct 1511

<210> 12

<211> 484

<212> PRT

<213> Homo sapiens

<400> 12

Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His

1	5	10	15
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Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20	25	30
----	----	----

Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Val Ser Asp Thr Tyr Lys

35	40	45
----	----	----

Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu

50	55	60
----	----	----

Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr

65	70	75	80
----	----	----	----

Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys

85	90	95
----	----	----

His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile

100	105	110
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Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser

115	120	125
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Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val

130	135	140
-----	-----	-----

Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg

145

150

155

160

Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu

165

170

175

Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr

180

185

190

Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg

195

200

205

Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln

210

215

220

Arg Thr Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr

225

230

235

240

Asp Ser Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys

245

250

255

Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro

260

265

270

Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly

275

280

285

Gly Gly Ser Gly Gly Pro Gly Gly Ala Ala Ala Ala Ala

290

295

300

Ala Leu Leu Gly Pro Asp Pro Ala Ala Ala Ala Leu Leu Arg Pro

305

310

315

320

Asp Ala Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly

325

330

335

Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Pro Phe Cys Leu Pro

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345

350

Phe Cys Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln Pro Phe

355

360

365

Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala

370

375

380

Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala

385

390

395

400

Ala Phe Pro Cys

405

410

415

Leu Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala

420

425

430

Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro

435

440

445

Gln His Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu

450

455

460

Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly

465

470

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Lys Glu Ala Pro

<210> 13

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<212> DNA

<213> Mus musculus

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<221> CDS

<222> (74)..(1303)

<400> 13

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acagccattg aac atg gac gaa gga atc cct cat ttg caa gag aga cag 109

Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln

1 5 10

tta ctg gaa cat agg gat ttt ata gga ctg gac tat tcc tct ttg tat 157

Leu Leu Glu His Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr

15 20 25

atg tgt aaa ccc aaa agg agc ttg aag cga gac gat acc aag gat acc 205

Met Cys Lys Pro Lys Arg Ser Leu Lys Arg Asp Asp Thr Lys Asp Thr

30 35 40

tac aag tta ccg cac aga tta ata gaa aag aag aga cga gac cga att 253

Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile

45 50 55 60

aat gaa tgc att gct cag ctg aaa gat tta ctg ccc gaa cat ctg aaa 301

Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys

65 70 75

ttg aca aca ctg ggg cat ttg gag aaa gca gta gtc ttg gaa tta act 349

Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr

80 85 90

tta aag cac ttg aaa gcg cta aca gcc tta act gag cag cag cat cag 397

Leu Lys His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln

95

100

105

aag ata att gct tta cag aat ggg gag cgc tct ctg aaa tcg ccg gtc 445

Lys Ile Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Val

110

115

120

cag gcc gac ttg gat gcg ttc cac tcg ggg ttt caa acc tgc gcc aaa 493

Gln Ala Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys

125

130

135

140

gaa gtc ttg caa tac ctc gcg cgc ttt gag agc tgg aca ccc agg gag 541

Glu Val Leu Gln Tyr Leu Ala Arg Phe Glu Ser Trp Thr Pro Arg Glu

145

150

155

ccg cgc tgc gca cag ctc agc cac ctg cat gcc gtg gcc acc cag 589

Pro Arg Cys Ala Gln Leu Val Ser His Leu His Ala Val Ala Thr Gln

160

165

170

ctc ctg acg cca cag gtg ccc tcc ggc agg ggc tct ggg cgc gcg ccc 637

Leu Leu Thr Pro Gln Val Pro Ser Gly Arg Gly Ser Gly Arg Ala Pro

175

180

185

tgc agc gcg ggg gct gcg gcc gcc tcg ggt ccc gag cgc gtc gcc cgc 685

Cys Ser Ala Gly Ala Ala Ala Ser Gly Pro Glu Arg Val Ala Arg

190 195 200

tgc gtg ccg gtc atc cag cgg act cag ccc ggc acg gag ccg gaa cac 733

Cys Val Pro Val Ile Gln Arg Thr Gln Pro Gly Thr Glu Pro Glu His

205 210 215 220

gac acg gac acc gac agc ggc tac gga ggc gag gcg gag cag ggc cgc 781

Asp Thr Asp Thr Asp Ser Gly Tyr Gly Glu Ala Glu Gln Gly Arg

225 230 235

gcg gcc gtc aag cag gag cca ccc ggg gac tcg tcg cct gcg ccc aag 829

Ala Ala Val Lys Gln Glu Pro Pro Gly Asp Ser Ser Pro Ala Pro Lys

240 245 250

agg ccg aag ctg gag gcg cgc ggc gcg ctc ctg ggc ccg gag ccc gcg 877

Arg Pro Lys Leu Glu Ala Arg Gly Ala Leu Leu Gly Pro Glu Pro Ala

255 260 265

ctg ctc ggc tcg ctc gtg gcg ctt ggc ggg ggc gcg ccc ttc gcg cag 925

Leu Leu Gly Ser Leu Val Ala Leu Gly Gly Ala Pro Phe Ala Gln

270 275 280

ccc gct gcc gcg ccc ttc tgc ctg ccc ttc tat ctg ctg tcg ccg tcc 973

Pro Ala Ala Ala Pro Phe Cys Leu Pro Phe Tyr Leu Leu Ser Pro Ser

285 290 295 300

gcc gcc gcc tac gta cag ccc tgg cta gac aag agc ggc ctg gac aag	1021		
Ala Ala Ala Tyr Val Gln Pro Trp Leu Asp Lys Ser Gly Leu Asp Lys			
305	310	315	
tat ctg tac ccc gcg gcg gcc gcg ccc ttc ccg ctg ctg tat ccc ggc	1069		
Tyr Leu Tyr Pro Ala Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly			
320	325	330	
atc cca gca gcg gcc gcc gct gct gct gcc gct ttc cct tgc ttg	1117		
Ile Pro Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu			
335	340	345	
tcg tcc gtg ctg tcg cca ccc ccg gag aag gcc ggc gcg acc gcc ggt	1165		
Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Thr Ala Gly			
350	355	360	
gcc ccg ttc ctg gcg cac gag gtg gcg ccc ccg ggg ccg ctg cgc ccc	1213		
Ala Pro Phe Leu Ala His Glu Val Ala Pro Pro Gly Pro Leu Arg Pro			
365	370	375	380
cag cac gcg cat agc cgc acc cac ctg ccg cgc gct gtg aac ccg gag	1261		
Gln His Ala His Ser Arg Thr His Leu Pro Arg Ala Val Asn Pro Glu			
385	390	395	
agc tct cag gaa gat gcc acg cag ccg gcc aag gac gcc ccc	1303		
Ser Ser Gln Glu Asp Ala Thr Gln Pro Ala Lys Asp Ala Pro			

400

405

410

tgaacccagc attccttcca gaacaggca gggggctccc gaggagtcgc cgggtttcca 1363

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<213> Mus musculus

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Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His

1

5

10

15

Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro

20

25

30

Lys Arg Ser Leu Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro

35

40

45

His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile

50

55

60

Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu

65

70

75

80

Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu

85

90

95

Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala

100

105

110

Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Val Gln Ala Asp Leu

115

120

125

Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln

130

135

140

Tyr Leu Ala Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Ala

145

150

155

160

Gln Leu Val Ser His Leu His Ala Val Ala Thr Gln Leu Leu Thr Pro

165

170

175

Gln Val Pro Ser Gly Arg Gly Ser Gly Arg Ala Pro Cys Ser Ala Gly

180

185

190

Ala Ala Ala Ala Ser Gly Pro Glu Arg Val Ala Arg Cys Val Pro Val

195

200

205

Ile Gln Arg Thr Gln Pro Gly Thr Glu Pro Glu His Asp Thr Asp Thr

210 215 220

Asp Ser Gly Tyr Gly Gly Glu Ala Glu Gln Gly Arg Ala Ala Val Lys

225 230 235 240

Gln Glu Pro Pro Gly Asp Ser Ser Pro Ala Pro Lys Arg Pro Lys Leu

245 250 255

Glu Ala Arg Gly Ala Leu Leu Gly Pro Glu Pro Ala Leu Leu Gly Ser

260 265 270

Leu Val Ala Leu Gly Gly Ala Pro Phe Ala Gln Pro Ala Ala Ala

275 280 285

Pro Phe Cys Leu Pro Phe Tyr Leu Leu Ser Pro Ser Ala Ala Ala Tyr

290 295 300

Val Gln Pro Trp Leu Asp Lys Ser Gly Leu Asp Lys Tyr Leu Tyr Pro

305 310 315 320

Ala Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Ala

325 330 335

Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu Ser Ser Val Leu

340 345 350

Ser Pro Pro Pro Glu Lys Ala Gly Ala Thr Ala Gly Ala Pro Phe Leu

355

360

365

Ala His Glu Val Ala Pro Pro Gly Pro Leu Arg Pro Gln His Ala His

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375

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Ser Arg Thr His Leu Pro Arg Ala Val Asn Pro Glu Ser Ser Gln Glu

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Asp Ala Thr Gln Pro Ala Lys Asp Ala Pro

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<212> DNA

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Synthesized Primer Sequence

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<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

<400> 16

agcctgtcga gcatcgctta

20